FIGURE 1

Clone LR4: hLH/CG Receptor Fusion with Thioredoxin Gene in pET32 Vector
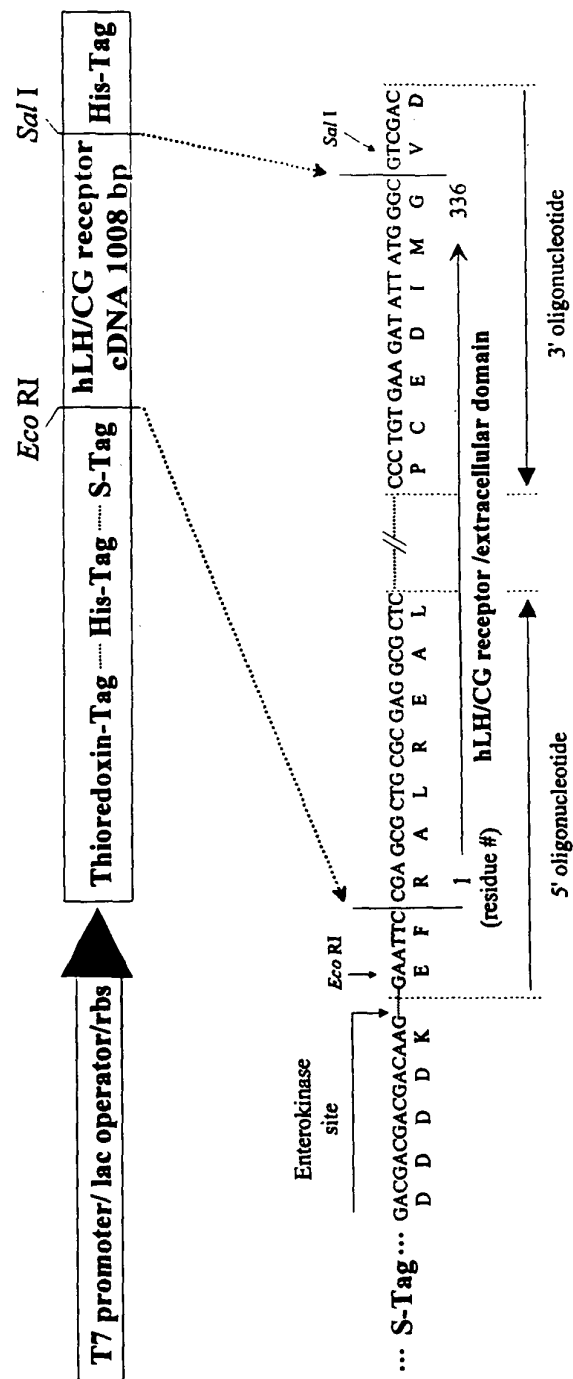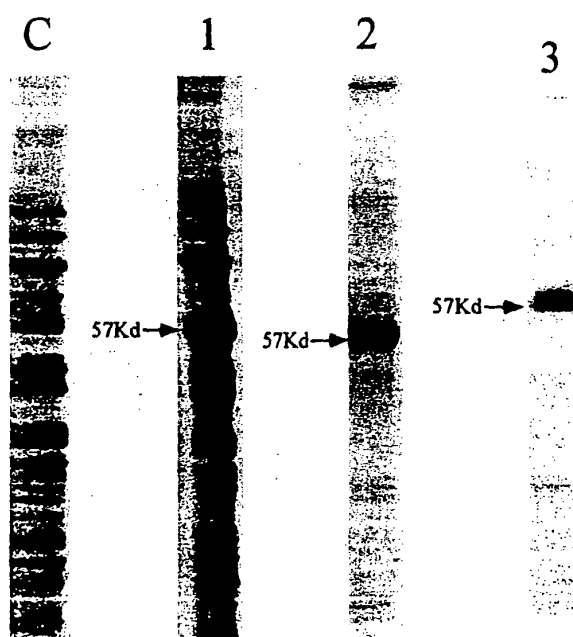
Thioredoxin-Tag ── His-Tag ── S-Tag | hLH/CG receptor cDNA 1008 bp | His-Tag

Eco RI

Sal I

T7 promoter/ lac operator/rbs

Enterokinase site

Eco RI

... S-Tag ··· GACGACGACAAG ── GAATTC ── CGA GCG CTG CGC GAG GCG CTC ──//── CCC TGT GAA GAT ATT ATG GGC GTCGAC
             D D D D K   E F   R A L R E A L   P C E D I M G   V D

1 (residue #)

336

hLH/CG receptor /extracellular domain

5' oligonucleotide

3' oligonucleotide

Sal I

FIGURE 2

Non-reducing protein gels

C   1   2   3

Panel A

57Kd→   57Kd→   57Kd→

Western blots

Murine anti-LHR   Monoclonal anti-
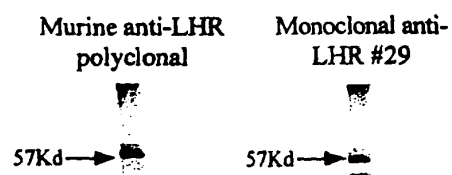polyclonal   LHR #29

Panel B

57Kd→   57Kd→

FIGURE 3

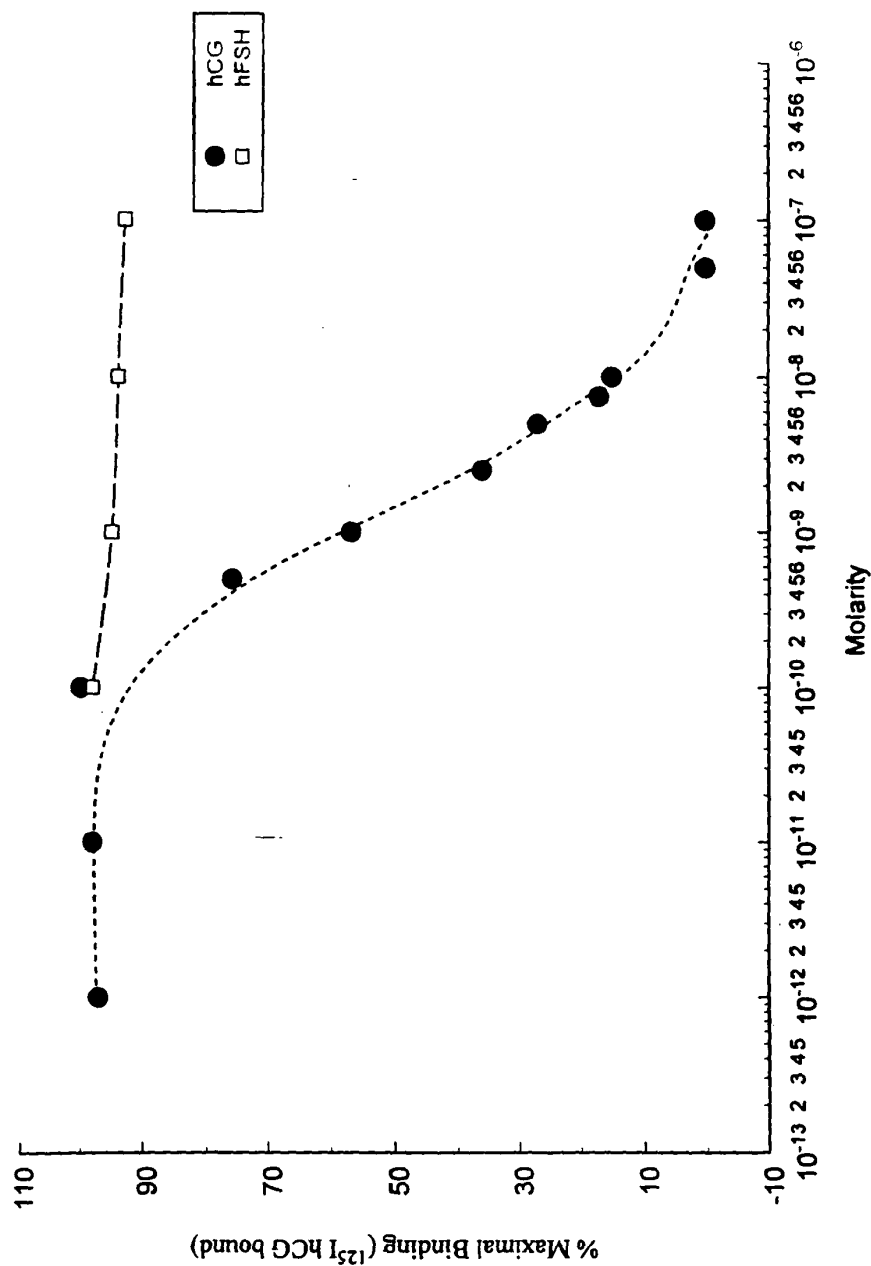Affinity of hLH/CG receptor fusion protein

FIGURE 4

Effect of anti-hCG monoclonal antibodies
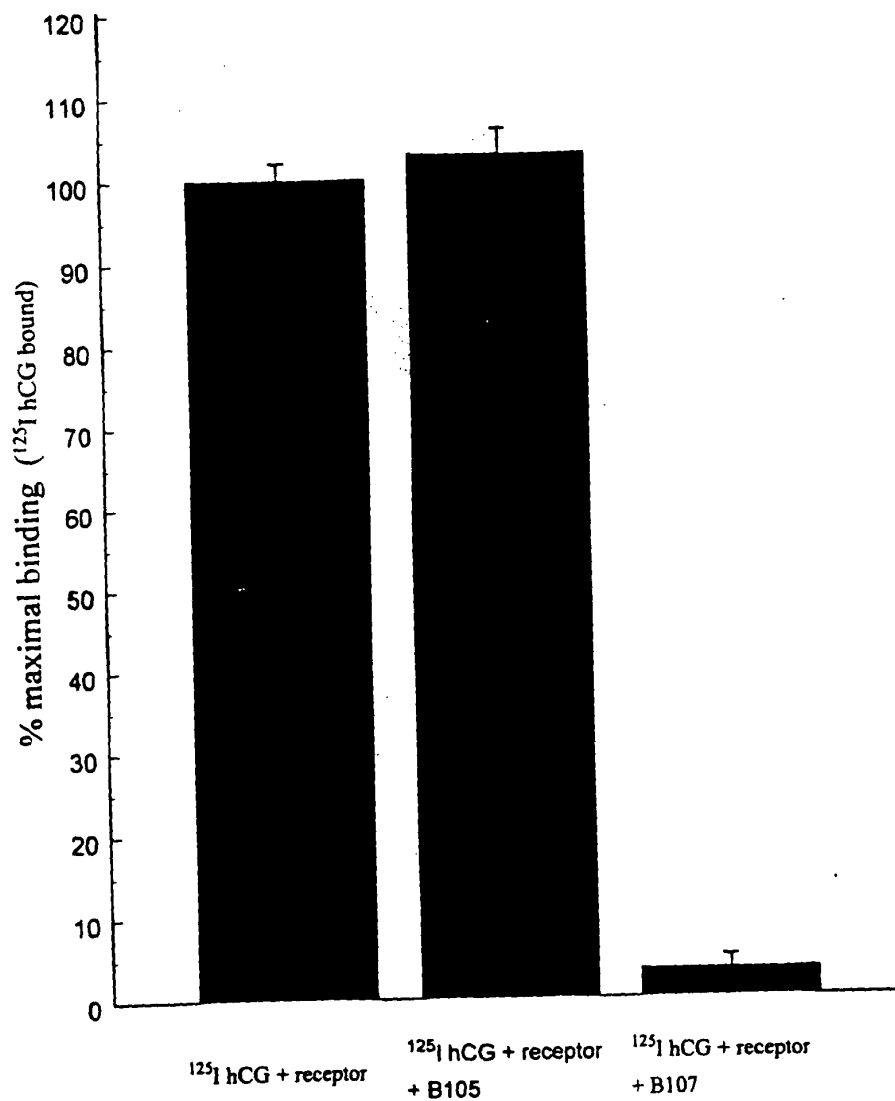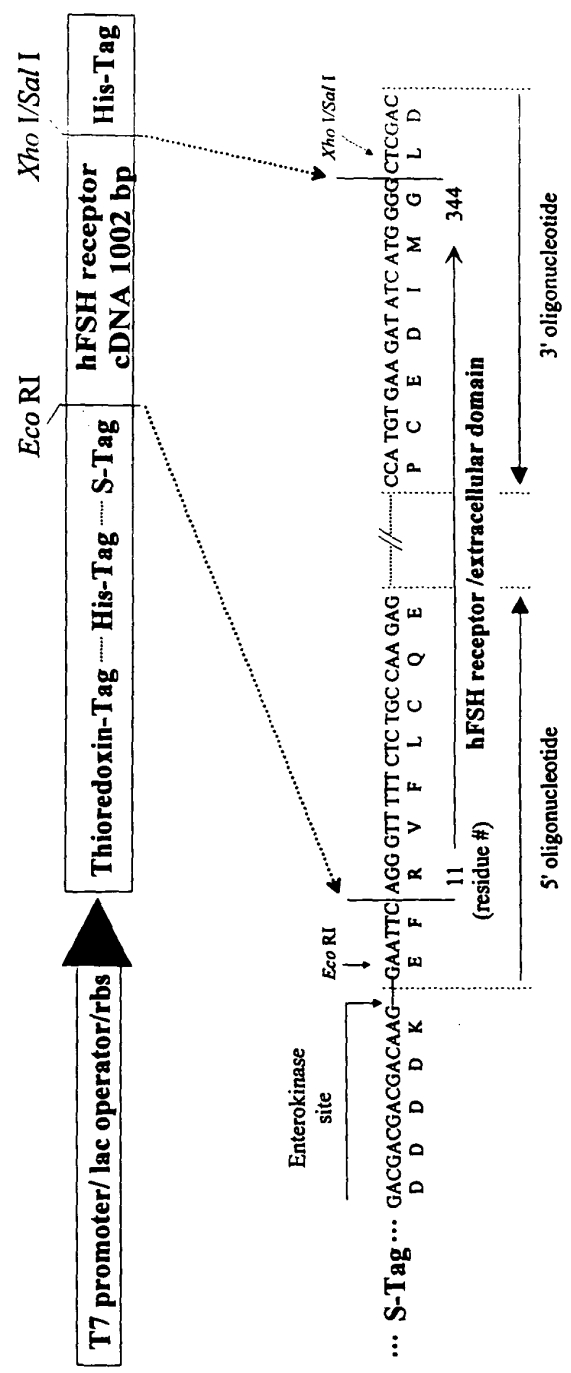on hCG binding to receptor fusion protein

FIGURE 5

hFSH Receptor Fusion with Thioredoxin Gene in pET32 Vector

Figure 6A

```
1    atgagcgataaaattattcacctgactgac
31   gacagttttgacacggatgtactcaaagcg
61   gacggggcgatcctcgtcgatttctgggca
91   gagtggtgcggtccgtgcaaaatgatcgcc
121  ccgattctggatgaaatcgctgacgaatat
151  cagggcaaactgaccgttgcaaaactgaac
181  atcgatcaaaaccctggcactgcgccgaaa
211  tatggcatccgtggtatcccgactctgctg
241  ctgttcaaaaacggtgaagtggcggcaacc
271  aaagtgggtgcactgtctaaaggtcagttg
301  aaagagttcctcgacgctaacctggccggt
331  tctggttctggccatatgcaccatcatcat
361  catcattcttctggtctggtgccacgcggt
391  tctggtatgaaagaaaccgctgctgctaaa
421  ttcgaacgccagcacatggacagcccagat
451  ctgggtaccgacgacgacgacaaggccatg
481  gctgatatcggatccgaattcagggttttt
511  ctctgccaagagagcaaggtgacagagatt
541  ccttctgacctcccgaggaatgccattgaa
571  ctgaggtttgtcctcaccaagcttcgagtc
601  atccaaaaaggtgcattttcaggatttggg
631  gacctggagaaaatagagatctctcagaat
661  gatgtcttggaggtgatagaggcagatgtg
691  ttctccaaccttcccaaattacatgaaatt
721  agaattgaaaaggccaacaacctgctctac
751  atcacccctgaggccttccagaaccttccc
781  aaccttcaatatctgttaatatccaacaca
811  ggtattaagcaccttccagatgttcacaag
841  attcattctctccaaaaggttttacttgac
871  attcaagataacataaacatccacacaatt
901  gaaagaaattctttcgtggggctgagcttt
931  gaaagtgtgattctatggctgaataagaat
961  gggattcaagaaatacacaactgtgcattc
991  aatggaacccaactagatgcagtgaatcta
1021 agcgataataataatttagaagaattgcct
1051 aatgatgttttccacggagcctctggacca
1081 gtcattctagatatttcaagaacaaggatc
1111 cattccctgcctagctatggcttagaaaat
1141 cttaagaagctgagggccaggtcgacttac
1171 aacttaaaaaagctgcctactctggaaaag
1201 cttgtcgccctcatggaagccagcctcacc
1231 tatcccagccattgctgtgcctttgcaaac
1261 tggagacggcaaatctctgagcttcatcca
1291 atttgcaacaaatctattttaaggcaagaa
1321 gttgattatatgactcaggctaggggtcag
1351 agatcctctctggcagaagacaatgagtcc
1381 agctacagcagaggatttgacatgacgtac
1411 actgagtttgactatgacttatgcaatgaa
1441 gtggttgacgtgacctgctcccctaagcca
1471 gatgcattcaacccatgtgaagatatcatg
1501 ggggtcgacaagcttgcggccgcactcgag
1531 caccaccaccaccaccactga
```

Figure 6B

```
  1 MSDKIIHLTDDSFDTDVLKADGAILVDFWA
 31 EWCGPCKMIAPILDEIADEYQGKLTVAKLN
 61 IDQNPGTAPKYGIRGIPTLLLFKNGEVAAT
 91 KVGALSKGQLKEFLDANLAGSGSGHMHHHH
121 HHSSGLVPRGSGMKETAAAKFERQHMDSPD
151 LGTDDDDKAMADIGSEFRVFLCQESKVTEI
181 PSDLPRNAIELRFVLTKLRVIQKGAFSGFG
211 DLEKIEISQNDVLEVIEADVFSNLPKLHEI
241 RIEKANNLLYITPEAFQNLPNLQYLLISNT
271 GIKHLPDVHKIHSLQKVLLDIQDNINIHTI
301 ERNSFVGLSFESVILWLNKNGIQEIHNCAF
331 NGTQLDAVNLSDNNNLEELPNDVFHGASGP
361 VILDISRTRIHSLPSYGLENLKKLRARSTY
391 NLKKLPTLEKLVALMEASLTYPSHCCAFAN
421 WRRQISELHPICNKSILRQEVDYMTQARGQ
451 RSSLAEDNESSYSRGFDMTYTEFDYDLCNE
481 VVDVTCSPKPDAFNPCEDIMGVDKLAAALE
511 HHHHHH*
```

Figure 7A

```
1 atgagcgataaaattattcacctgactgac
31 gacagttttgacacggatgtactcaaagcg
61 gacggggcgatcctcgtcgatttctgggca
91 gagtggtgcggtccgtgcaaaatgatcgcc
121 ccgattctggatgaaatcgctgacgaatat
151 cagggcaaactgaccgttgcaaaactgaac
181 atcgatcaaaaccctggcactgcgccgaaa
211 tatggcatccgtggtatcccgactctgctg
241 ctgttcaaaaacggtgaagtggcggcaacc
271 aaagtgggtgcactgtctaaaggtcagttg
301 aaagagttcctcgacgctaacctggccggt
331 tctggttctggccatatgcaccatcatcat
361 catcattcttctggtctggtgccacgcggt
391 tctggtatgaaagaaaccgctgctgctaaa
421 ttcgaacgccagcacatggacagcccagat
451 ctgggtaccgacgacgacgacaaggccatg
481 gctgatatcggatccgaattccgagcgctg
511 cgcgaggcgctctgccctgagccctgcaac
541 tgcgtgcccgacggcgccctgcgctgcccc
571 ggccccacggccggtctcactcgactatca
601 cttgcctacctccctgtcaaagtgatccca
631 tctcaagctttcagaggacttaatgaggtc
661 ataaaaattgaaatctctcagattgattcc
691 ctggaaaggatagaagctaatgcctttgac
721 aacctcctcaatttgtctgaaatactgatc
751 cagaacaccaaaaatctgagatacattgag
781 cccggagcatttataaatcttccccgatta
811 aaatacttgagcatctgtaacacaggcatc
841 agaaagtttccagatgttacgaaggtcttc
871 tcctctgaatcaaatttcattctggaaatt
901 tgtgataacttacacataaccaccatacca
931 ggaaatgcttttcaagggatgaataatgaa
961 tctgtaacactcaaactatatggaaatgga
991 tttgaagaagtacaaagtcatgcattcaat
1021 gggacgacactgacttcactggagctaaag
1051 gaaaacgtacatctggagaagatgcacaat
1081 ggagccttccgtggggccacagggccgaaa
1111 accttggatatttcttccaccaaattgcag
1141 gccctgccgagctatggcctagagtccatt
1171 cagaggctaattgccacgtcatcctattct
1201 ctaaaaaaattgccatcaagagaaacattt
1231 gtcaatctcctggaggccacgttgacttac
1261 cccagccactgctgtgcttttagaaacttg
1291 ccaacaaaagaacagaatttttcacattcc
1321 atttctgaaaacttttccaaacaatgtgaa
1351 agcacagtaaggaaagtgaataacaaaaca
1381 ctttattcttccatgcttgctgagagtgaa
1411 ctgagtggctgggactatgaatatggtttc
1441 tgcttacccaagacaccccgatgtgctcct
1471 gaaccagatgcttttaatccctgtgaagat
1501 attatgggcgtcgacaagcttgcggccgca
1531 ctcgagcaccaccaccaccaccactga
```

Figure 7B

```
  1 MSDKIIHLTDDSFDTDVLKADGAILVDFWA
 31 EWCGPCKMIAPILDEIADEYQGKLTVAKLN
 61 IDQNPGTAPKYGIRGIPTLLLFKNGEVAAT
 91 KVGALSKGQLKEFLDANLAGSGSGHMHHHH
121 HHSSGLVPRGSGMKETAAAKFERQHMDSPD
151 LGTDDDDKAMADIGSEFRALREALCPEPCN
181 CVPDGALRCPGPTAGLTRLSLAYLPVKVIP
211 SQAFRGLNEVIKIEISQIDSLERIEANAFD
241 NLLNLSEILIQNTKNLRYIEPGAFINLPRL
271 KYLSICNTGIRKFPDVTKVFSSESNFILEI
301 CDNLHITTIPGNAFQGMNNESVTLKLYGNG
331 FEEVQSHAFNGTTLTSLELKENVHLEKMHN
361 GAFRGATGPKTLDISSTKLQALPSYGLESI
391 QRLIATSSYSLKKLPSRETFVNLLEATLTY
421 PSHCCAFRNLPTKEQNFSHSISENFSKQCE
451 STVRKVNNKTLYSSMLAESELSGWDYEYGF
481 CLPKTPRCAPEPDAFNPCEDIMGVDKLAAA
511 LEHHHHHH*
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